REMARKS/ARGUMENTS

This is in response to the Office Action mailed February 18, 2010 for the above-captioned application. An extension of time sufficient to make this paper timely is requested and the appropriate fee is enclosed.

Claims 62-64 and 74 have been canceled without prejudice or disclaimer. Claims 65-71, 73, 75, and 76 are amended. Claims 77-82 are added. No new matter has been added. Therefore, claims 65-73 and 75-82 are now pending. Claims 65, 69, 71, 75, and 77 are independent claims.

Claims 62-76 stand rejected under 35 U.S.C. § 112, first paragraph, as failing to comply with the written description requirement. Of these claims, claims 65-73, 75, and 76 remain pending. Based on the Examiner's statement of the claim interpretation to support the claim rejection, Applicants believe that the amendments made herein fully address the rejection as directed to the claims.

With respect to claims 65-68, the Office alleges that "[t]he structural features that distinguish those nucleic acids that modify the levels of chalone synthase, dihydroflavonal 4-reductase and leucoanthocyanidine reductase in a plant cell from those that do not are not described in the specification." Applicants respectfully disagree, as these structural features are shown in the sequences and plasmid maps disclosed. Further, pages 5 and 6 of the originally filed Specification discuss conservative amino acid substitutions. *See* Specification at paragraphs [0022] and [0023]. For the Examiner's convenience, nucelotide and amino acid alignments of TrCHS3a, TrCHSc, TrCHSf and TrCHSh, as well as TrLARa, TrLARb and TrLARc, identifying conserved regions are included as Appendix A.

Claims 62-76 also stand rejected under 35 U.S.C. § 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter that Applicant regards as the invention. In view of the amendments made herein, Applicants respectfully request reconsideration and withdrawal of this rejection.

With respect to the recitation of "dihydroflavonal 4-reductase (BAN)," Applicants respectfully submit that, at the time the present application was filed, BAN was thought to be DFR-like, hence the nomenclature used in the patent application. BAN is now thought to be a member of the ANR family of genes. BAN is the nomenclature given to the flavonoid biosynthetic gene, Banyuls, in *Arabidopsis thaliana*, but it is used somewhat loosely in the literature. Anthocyanidin reducatase (*ANR*) is the name now given to the homolog of BAN in *Trifolium repens (TrANR)*. *TrLAR* (Leucoanthocyanidin 4 reductase) is another very closely related *T. repens* gene. ANR is a more generic term.

Claims 65 and 67 stand rejected under 35 U.S.C. § 102 as being anticipated by Suzuki et al. (2000, Mol. Breed. 6:239-246). The Examiner stated that the basis for this rejection was that the sequences disclosed by Suzuki would have a at least a portion that is 90% identity to "the relevant part" of 2. 4. 6. or 8 and at least 90% identity to the "relevant part" of SEQ ID NO: 10, and are at least 60 nucleotides long. However, this rejection is based on the construction of the fragment length as being as few as two bases. The amendment of Claims 65 and 67 is believed to overcome this rejection.

Claims 62-76 stand rejected under 35 U.S.C. § 103 (a) as being unpatentable over Spangenberg et al. (U.S. Patent Application Publication No. 2005/0069884). However, Spangenberg is disqualified as prior art under 35 U.S.C. § 103(c). 35 U.S.C. § 103(c)(1) states:

> Subject matter developed by another person, which qualifies as
> prior art only under one or more of subsections (e), (f) and (g) of
> section 102 of this title, shall not preclude patentability under this
> section where the subject matter and the claimed invention were, at
> the time the claimed invention was made, owned by the same
> person or subject to an obligation of assignment to the
> same person.

For the purposes of 35 U.S.C. § 103(c), a "person" may be a corporation. Spangenberg et al. could qualify as a prior art reference only under 35 U.S.C. § 102(e), and both Spangenberg et al. and the present pending application were under an obligation of assignment to Agriculture Victoria Services Pty Ltd. and Agresearch Limited at the time the claimed invention was made. Thus, Spangenberg et al. does not qualify as prior art per 35 U.S.C. §103(c). Accordingly, this rejection is improper and must be withdrawn.

Claims 62-76 stand rejected under 35 U.S.C. § 103(a) as being unpatentable over Dixon et al. (U.S. Patent Application Publication No. 2004/0093632) in view of Arioli et al. (1994, Gene 138:79-86. Dixon et al. describes plants transformed with a LAR (which Dixon et al. calls a BAN gene) and mentions in paragraph [0062] the possibility of a DFR/LAR combination. The Examiner also alleges that the Dixon et al. at paragraph [0010] teaches a combination of chalcone synthase with LAR. However, Dixon et al. refers to chaclone isomerase, rather than chalcone synthase. Chalcone isomerase is a different enzyme from chalcone synthase, and has different specific activity acting on a different substrate.   For at least these reasos, the combination of Dixon et al. and Arioli et al. fails to obviate claims 65-76, or newly added claims 77-82.

     In view of the foregoing, Applicants submit that all of the claims of this application are now in form for allowance, and such action is respectfully urged.

Respectfully submitted,

/Allison Olenginski/ _____

Marina T. Larson, Ph.D
Attorney/Agent for Applicant(s)
Reg. No. 32038

Allison Olenginski
Attorney/Agent for Applicant(s)
Reg. No. 55509

(970) 262-1800

TrCHS nucleotide sequence alignment

```
TrCHS3as : GAATTCACTAGTGATTAAGCAGTGGTAACAACGCAGAGTACGCGGGCAA-----CAAAAA :
55
TrCHScs  : GAATTC------GATTAAGCAGTGGTAACAACGCAGAGTACGCGGGCATT----CAATCT :
50
TrCHSfs  : GAATTC------GATTAAGCAGTGGTAACAACGCAGAGTACGCGGGACT------AAGCC :
48
TrCHShs  : GAATTCACTAGTGATTAAGCAGTGGTAACAACGCAGAGTACGCGGGCGAATCCACCAAAT :
60

TrCHS3as : CAACTACG------------CATATTATATAATATAT----ATAAAAGTCTATAATTCAA :
99
TrCHScs  : GTTGTGCAT-AAAATTCACTCATTGCATAGTAAAACATACACATTTGAACGTTGCAAGAA :
109
TrCHSfs  : TTGATTCAT----------TGTTTGTTTCATAAACACA--AGAACTAGTGATTGCTTCTA :
96
TrCHShs  : CAACACCATTAATAACCTTCCAAATTCTCGTTACCTCACCAAATCTCATTTTCATTATA :
120

TrCHS3as : AGAAACTGCTAAAGATATTA---TTA----------AGATAT--GGTGAGTGTAGCTGAA :
144
TrCHScs  : GAAATATGGGAGACG----------A----------ACGTAT--AGTGAGAGGTG----- :
142
TrCHSfs  : TCTTAAGAAAAAATGCCTCAAGGTTGATTTGAATGGAACTTCCTCCGGTGAATGGAGC--AC :
154
TrCHShs  : TATCTTGCGGTACATCTCTTTTG---TTACCTCCAACAAGAAAAT--GGTGACCGTAGAAGCG :
175

TrCHS3as : AATCGCTAGCTTCTGAGGGGTGAAGCCCTGCTACCATTTTGGCCATTGGTACTGCAAAT :
204
TrCHScs  : -T-CACTAAGT--TGACAACCCCTGCCAAGCGTACTATATTCGCTCTTGGCAAGGCATTC :
198
TrCHSfs  : GAGCTAGACGTG-CTCCTACTCAGGCAAAGCCAACGATACTTGCATTAGGCAAAGCTTTC :
213
TrCHShs  : ATTCGTAACGCCCAACGTTCAAATGGCCCCTGGCACTATCTTAGGTTTTGGCACAGCCACT :
235

TrCHS3as : CCACCAAACCGCTGTTGAGCAGCAGCACAA-ATCCTGATTTCTACTTCAAAATTACAACAG :
263
TrCHScs  : CCTCACCAACTTCTTGATGCA-AGAGTGCTTTAGTTGATGGTTATTTTACGGAGACTAATTG :
257
TrCHSfs  : CCCGCCCAGGTCCTTCCCTCA-AGAGTGCCTGGTGGAAGGATTCATTCCGACGACTAAGTG :
272
TrCHShs  : CCTTGTAACTGTGTTCACTCA-AGCTGATTTATCCTGATTACTACTTTCCTATCACCAACAC :
294

TrCHS3as : TTGAGCACAACGACTGAGCTCAAATATAAGTTCCAACCCATCTGTGACAATCCATCATCAA :
323
TrCHScs  : TTG---ACAATCCTTAACTTAAGCAGAAACGTTGCTACACTTTGTAAGACGACGACGCAAA :
314
TrCHSfs  : TTG---ACGATACTTATATTAACGAGAAATTGGAGCGTCTTTCCAAAAACACAACTGTTGAA :
```

```
       329
TrCHShs  : CGAACATATGACTGATCTTAAGTAAAAATTCAAGCGGATGTGCATAGTCGTATGATTAAA :
       354

TrCHS3as : GAGCAGATACATGTATCTAACAGAAGAGATTTTGCAAGAAAATCCTAGTCTTTGTCAATA :
       383
TrCHScs  : AACAAGGTATGTTGTTATGCATGACGAUATACTAAAGAAATATCCTGTAGTTGTCGTCGA :
       374
TrCHSfs  : AACAAGATACACAGTAATTGTCAACGAGATCTTAGCAACTATCCACGTGGTAGCCATAGA :
       389
TrCHShs  : CAAACGTTACATGCACCTAACAGAAGACTTTTCTGTAGGAGAATCCCAATTATGTGTCAATTA :
       414

TrCHS3as : CATGCCACCTTCATTGGATGCTAGCCATGACATGCTGGTGCTTGAGGTACCTAGACTTCG :
       443
TrCHScs  : AGGCTCCTCAACTGTTAAACAACCTTTTAGACATATGTAATCAGCTAGTAAGACTAATCGC :
       434
TrCHSfs  : TGGAACACCTACTATTAGGCAATAGCTTTGAAATAGCAAACTCCACGTAGTTGTCAATCGC :
       449
TrCHShs  : CATGTCTCGCCATCACTTCGATGTTAAGCATGGAGACATACTGGTTCTTGAAGTACCAATGCCTACG :
       474

TrCHS3as : GAACGACGTGCAGTCATGGCCATTAAATGAATGGGGTCAACCAAAGTCAAAGATTACTCA :
       503
TrCHScs  : AATTGAAGCTTGCCCAAGTTTGCCTAAAGAATTGGGGTAGATCCTTATCGGACATAACTCA :
       494
TrCHSfs  : AACAAGCGCAAGCAAAGATTGCATCAAACGAATGGGGAAGGTCACCTCAAGATATCACACA :
       509
TrCHShs  : TAAAATGCAGCAAATAAAAGCCATATGTGAATGGGGACAACCAAAATCCAAAAATCACACA :
       534

TrCHS3as : CTTAAACTTTTGCACCACCAAGTGGTGCTTGACATGCCTGGCGCTGATTACCAAGTCACTAA :
       563
TrCHScs  : TGTCGTTTTATGTTTCATCTAGTGAAGCTAGATTACCGGCTGCTGACCTATACTTGTCTAA :
       554
TrCHSfs  : CATAGTCTATGTTTCTTCGGAGCGAAATTCGTCTTACCCGGTGCTGACCTTTATCTTGCTAA :
       569
TrCHShs  : TCTTCGTTTTCTGCACCCACTTCCCGTGTTTGACAACGCCGGCAGCCGATTACCAAGTCACGCAA :
       594

TrCHS3as : ACTCTTTGGTCGTCGCCCATATGTACGAAAGGTATATGCAGCTACCAACAAGGTTGTTTTGC :
       623
TrCHScs  : AGGACTTGGCAGTAAACCCTAGAAATTCAAACAAAACCATGCTGTATTTCTCTCGGATCGTCGTCGG :
       614
TrCHSfs  : TGAACTCGCCTTAAACGAGCGATGTTAATCGCGTAATGCTCTATTTCCTCCGGTTGCTACGG :
       629
TrCHShs  : ACTTTTTAGGCTTAAAACCTTCTGTCAAGCGTCTCATGATCTATCAACAAGGTTGTTTCGC :
       654

TrCHS3as : AGGAGGCACGCGTCGTTCGTTTGCGCAAAGATTTGCCCGACAACAACAAAGTACCTCSTGT :
       683
TrCHScs  : AGGCCTAGCCGCGGCTTCCGTTGCCAAAGACGTAGCTGAGAACAACCCTGCAAGTACAGT :
       674
TrCHSfs  : CCGTGTCACTGCGCTTACGTGTGCGCAAAGACATCGCGCGAAAATAACCCTGGTAGTACGGT :
       689
TrCHShs  : TCGCGGCACACTTGTCCGCTTAGCAAAAGACCTTCTTTGAGAATAACAAAAATGCAAGAGT :
       714

TrCHS3as : GCTAGTTGTTTGTTCTGAGGTCACCGCAGTCACATTTCCCGGCCCAGTGATAGTCACTT :
```

```
743
TrCHScs    : TTTGCTTCCTACTTCCGAAACTAGAATTATTGGATTCAAGCCACCAACTCTTGATAGAGCC :
734
TrCHSfs    : GTTACCCACAACATCCGAGCCCAGTATTCTCGGTTTTCCACCACCCAGTAAAGCTTAGACC :
749
TrCHShs    : TCTTGTTTCTATCTTCTGAAATTACTGCCGGTTACTTTTCCTGGACCATCGGATAGTCATGT :
774

TrCHS3as   : GGACAGTCTTGTTCGACAAGCATTCTTTCGGAGATGGAGCCGCTGCACTAATTGTTCCTTC :
803
TrCHScs    : TTATCGATCTTGTTCGGTGTGCCACTCTTTGGAGATGGTGCTCGTGCAATCATAATTGGCTC :
794
TrCHSfs    : TTATGACCTCGTTGGCGCGTGCACTTTTTCGGTGATGGCGCCGCTGCTGCAATAATTGGAAC :
809
TrCHShs    : TGAATCGCTCGTCGGACAGCGCCGTTTTTGGTGATGGAGCCGCACTAATCATCATTATTGGTGC :
834

TrCHS3as   : TGATCCAGTGCCTGAAATTGACAACCCAATATTTGACATCGTTTGGACTGCACAAACAAT :
863
TrCHScs    : AGAACCCGTTATTTGAAACTGACACCCCATACTTTGACGTCCACACTTCACGTCAGGAGTT :
854
TrCHSfs    : AGACCCTACATTGAATCAAGAATCCCGTTTCATCGCAATTCAACCATCCAGTCCAAAAATT :
869
TrCHShs    : GGATCCTCATTTAACCGTCGACCGTCCGATTTCCACGATTGTTTCCGCTCCTCAGACTAT :
894

TrCHS3as   : TGCTCCTGACAGTGAAGGTCCCATTGATGCTCATCTTCGTGACGCTGGGCTAACATTCA :
923
TrCHScs    : TATACCAGACACCCACAAGAAAATTGATGCGCGCGTGACGGAGGACGGCCATAAGCTTCAC :
914
TrCHSfs    : CTTGCCTGATACACAAAATCTGCATTGATGCGTAGAATCACGATGACGGTATTAACTTTAA :
929
TrCHShs    : TCTTCCTGATTCTGATGGCCCAATTGATGGCACATCTTCCGTGACGTCGGCGCTCACTTTTCA :
954

TrCHS3as   : TCTTCTTAATGATGTTCGTGGCAATTGTATCAACGAACATTAA----------TAAAGCATT :
974
TrCHScs    : ACTTAGCAAGGGAACTTCCGCAGACAATCGAACACACATCGTTCAGGGATTCTGTAATAAACT :
974
TrCHSfs    : GTTTGGAAGTGACCTTCGTCAAAAAATTGAAGACAATCTTTAA----------AGAATTTT :
979
TrCHShs    : TTAATTGAATGATGTTCGGGGCATTATTTCAAAGAACGTTTAA----------AAAAAGTTA :
1005

TrCHS3as   : GGTTGAGCGTTTCCAACCA-TTACGAATTTCTGACTACAACTCAATCTTTTGGCATTCCAC :
1033
TrCHScs    : AATTGATGTTGTTGGG----TTGCAGAAATAACGAGTACAATAAGTTGTTTTGGCGTGTGC :
1030
TrCHSfs    : GCAAGAAAATTATCGCTAAAAGTGCATGTTAACGATTTAATGACTTATTTTGGCCTGTTC :
1039
TrCHShs    : AGTTGAAGCTTTTGCGCCT-ATTGCGGATTAATGATAGGAACTCAATATTTTGGCTTGCAC :
1064

TrCHS3as   : ACCCCGGTGGCACCTGCAATTCTTGCATCAAGTAGATCACAACAAGCTAGCCTTGAACGCCCCTAAA :
1093
TrCHScs    : ATCCAGGTGGCCCTGCCATATTGAATCGCCTTGGAGACAGCCGCCTTGTACTTGTCGCCCGCAGA :
1090
TrCHSfs    : ATCCTAGGTGGCCCAGCTATACTCAATAAGCTAGAAGAAATATACTCAAATTGACAAAGTGATA :
1099
```

```
TrCHShs  : ATCCAGGTGGACCGGCTATTTTAGACCACGTTGATGAGTAACTCCATCTTATAGAGGAGA :
1124

TrCHS3as : AGATCAGGGCCACGACGGAAGTTCTTAGTGTATATGGAAACATGTCAAGCCCATGTGTAT :
1153
TrCHScs  : AGCTCAATCGTAGTGCGAAAAGCTGTTATCGATTATGGAAA---TGCTGCCAGCAATACTAT :
1148
TrCHSfs  : AATTGGATTGTAGTGCGAAGGCATTTATCGATTATGGAAA---TGTTTAGTGGCAATACTAT :
1157
TrCHShs  : AACTCCGGTGCACCCGCCATCGTGCTTAGTGATATGGAAATATGTCAAGTCGCATGTGTTT :
1184

TrCHS3as : TGTTCATCT---TACATGCGATCCGAAGTAAACCGCTCAAAATCCACTTTAGACTAACTGG :
1211
TrCHScs  : TGTTTATCT--GCTGGAATATATGCTAGTACGA-GCAAAAGAAGATTGAAAAGCCGGGTGC :
1205
TrCHSfs  : ATTCTATCTGATCGAGTATATGCACAGATTATTTGAAGGAAGATCGAAGTGCAGATGGGC :
1217
TrCHShs  : TATTTATTT--TTGCATGAAATGCAGAAAGAGGTCTACAGAGAGGAACGCATGTATTACAACTGG :
1242

TrCHS3as : AGAAGGACTTGATTGCGGCTGCTGTTGTTCCGCTTCCGA--------CC-----AGCCACTTA :
1258
TrCHScs  : ACGCAGATACTGTATTGGGGGATTGATACATTGCTTTTGGA--------CC-----TGCCAATTA :
1252
TrCHSfs  : ATTTAGCATTGCCTTTTGGACCAGGCGATTACTTTTGAAGGGGTTCTGCTCCGTAGCCTTTA :
1277
TrCHShs  : TCAAGGGCTAGGAATCGGGTGTGTTGTTTGGGTTTGGA--------CC-----GCGTTTTA :
1289

TrCHS3as : GCATTGAAACCGTTGTTGTTCGTA----SCTTCGT-------------------------T :
1290
TrCHScs  : CTTTTGAGGGGATTCTAGCAAGGACTTGTGTTCCATGAAGTCTTATACG-----ATTGTG :
1307
TrCHSfs  : ATCTTGAATTAATAATTCATATGAATTACTTCTGTTAAGATTGTGATGGGAAGATGAAT :
1337
TrCHShs  : CTAGTTGAAACCGTTGTCGTTCATA----GTCTTCCGGTTCAGGGTTGAA-----TTTATT :
1340

TrCHS3as : ATATA-------------------------------AGATCTG---------------- :
1302
TrCHScs  : ATGCATGACTT--ATACTCTTATT---TCTACTAATTATTATTTTAGCAAATTCAG--- :
1359
TrCHSfs  : ATGTATTGGATTAATATTGATATTGGTGTTATTTAAGTTCATTTTAAAATAAGTTATTA :
1397
TrCHShs  : ATACATAGATTGGGAAAATAAAATT---TGCCTGCCGAGACATGTGAACTAACTTAGT--- :
1394

TrCHS3as : ---------------------------TGA----------------TTGTTTTTAT-- :
1315
TrCHScs  : ---AACTTTTAAGTAA---TGATTTAATGAAGAATACTTATAGTATATTAA-CTTTAATC :
1412
TrCHSfs  : ATACAGTATGATGTACCAATTGTTGTTTGAATGTTAAAAGGGAAGTATACTATTTTAAGT :
1457
TrCHShs  : ---AGGCAAGCTCAATT--TTAAAGTTTGAGG-ATAAATATTGTGCTTTAGT-TATTATGG :
1445

TrCHS3as : --TTTTAATGTATTACTTTTAATCTTGCTGC----C-----------TTGAATTTCT--AAT :
```

```
1357
TrCHScs  : ACTTTCGAAGCAACTTTATGATCCTAA--GACATGG----------TACACATTGAGCATG :
1461
TrCHSfs  : TCTTGACCATACTGATTTTTTCTTTACACATTTTCATATCTAAAATTGTTCTATCATATC :
1517
TrCHShs  : TATGTATTGTTATGTTTTTACCTTTTTCGTAATTC----------ATGTCAATTC--ATA :
1493

TrCHS3as : T-----------A-TG-TTTA--------------------------AATTAAATATACTTT :
1380
TrCHScs  : TGGA--------ATTGTTGTTAACAAAAACACTA-------------AGCGAATACAGACTT :
1501
TrCHSfs  : TTCATTGTTGATACTGTAATAATATAATATCTAATTTGGCTGGCAATATGATACGATTTTT :
1577
TrCHShs  : TGTA--------A-AGTATATGTTTGGGTTGG------------ATTATATTATTTTGTT :
1532

TrCHS3as : TGA-TAATAAAAAATAA-----AAAAAATAAAAAAAAAAAGTACTCTGCGTTGTTACCACTG :
1434
TrCHScs  : TATGTAGTATAAAGCATTTCCAGACATGATAAATAATGTAC-CTCACAACATAAATAT :
1560
TrCHSfs  : CACCGAAAATAAAATAAAA---AAATAAAAAAAAAAAAGTACTCTTCGTTGTTACCACTG :
1634
TrCHShs  : TAACTAAAAAAAKAA--------AAAAAATAAAAAAAAAAGTACTCTGCGTTGTTACCACTG :
1587

TrCHS3as : GTTTAATCGAATTC---------------------------------------------- :
1447
TrCHScs  : ATTTTAGCTATCTTCATCCCCAACTTTACACATCCACCAAGGTACAGAATAAGCATATGT :
1620
TrCHSfs  : GTTTAATCACTAGTGAATTC--------------------------------------- :
1653
TrCHShs  : GTTTAATCGAATTC---------------------------------------------- :
1600

TrCHS3as : --------------------------------------------------------------- :
-
TrCHScs  : CAACACAAAATGTACTCTAAGTCTAACATGAGTAACCAAACATGATGCCTGATTAAGTTA :
1680
TrCHSfs  : --------------------------------------------------------------- :
-
TrCHShs  : --------------------------------------------------------------- :
-

TrCHS3as : --------------------------------------------------------------- :
-
TrCHScs  : AAAGAAAAGAAAATCTGAGGGCATAGATCTTCAATCACACCACTCCAGAGGGAAGGCGTA :
1740
TrCHSfs  : --------------------------------------------------------------- :
-
TrCHShs  : --------------------------------------------------------------- :
-

TrCHS3as : --------------------------------------------------------------- :
-
TrCHScs  : GAACAAGCTGTCCGCCGAAAACACTGCAATTCAATAAATATCATTAGGACAACAGTGCAG :
1800
TrCHSfs  : --------------------------------------------------------------- :
-
TrCHShs  : --------------------------------------------------------------- :
-
```

```
TrCHS3as :  ------------------------------------------------------------ :
-
TrCHScs  : AGTCATGCGGGAAATGTCTTAAGTCACTGTACTAAAAATATAGGATTATATTATGAACTA :
1860
TrCHSfs  : ------------------------------------------------------------ :
-
TrCHShs  : ------------------------------------------------------------ :
-


TrCHS3as :  ------------------------------------------------------------ :
-
TrCHScs  : TACTAACCTTTTCACATAATAGTAACAGAAATCAGCTAAGATGAATGTCTGGACAATTTC :
1920
TrCHSfs  : ------------------------------------------------------------ :
-
TrCHShs  : ------------------------------------------------------------ :
-


TrCHS3as :  ------------------------------------------------------------ :
-
TrCHScs  : TGAGATAAGAACCATGACGGCCATAAGCCATACCCCAAGGCAACCAATAAATGTCCACGG :
1980
TrCHSfs  : ------------------------------------------------------------ :
-
TrCHShs  : ------------------------------------------------------------ :
-


TrCHS3as :  ------------------------------------------------------------ :
-
TrCHScs  : GTATCTAACACCTGTTGCAAGAAATAGTAAGTTATTAGGAGATGTGCGGTTACGAAATTC :
2040
TrCHSfs  : ------------------------------------------------------------ :
-
TrCHShs  : ------------------------------------------------------------ :
-



TrCHS3as :  ------------------------------------------------------------ :
-
TrCHScs  : AAGCTACACAACAAAAGGAGGCCAGAACAACAGCAATCTTGTAACCAGATGACAACAATA :
2100
TrCHSfs  : ------------------------------------------------------------ :
-
TrCHShs  : ------------------------------------------------------------ :
-


TrCHS3as :  ------------------------------------------------------------ :
-
TrCHScs  : AAATGTAAACTTAAAGAGACCGAACACACAAACATTGCAACTCAGATGGAATTGCTGCCA :
2160
TrCHSfs  : ------------------------------------------------------------ :
-
TrCHShs  : ------------------------------------------------------------ :
-


TrCHS3as :  ------------------------------------------------------------ :
-
```

```
TrCHScs   : TGTAACTAGTAGGAGATTTGGGACGTCAAATCAGTATATTATGCAAATACAAGGTATGAC :
2220
TrCHSfs   : ------------------------------------------------------------ :
-
TrCHShs   : ------------------------------------------------------------ :
-


TrCHS3as  : ------------------------------------------------------------ :
-
TrCHScs   : CGCCTTGTCTATTGTAGCATACAACAAACGTACAGTGGGTTTGTCCCTCTCAAAATGGCA :
2280
TrCHSfs   : ------------------------------------------------------------ :
-
TrCHShs   : ------------------------------------------------------------ :
-


TrCHS3as  : ------------------------------------------------------------ :
-
TrCHScs   : GGATCTTTACAGCACAATATTTGGTTTTGTCATACTTATACCATAAAAAAAAAAAAAAAA :
2340
TrCHSfs   : ------------------------------------------------------------ :
-
TrCHShs   : ------------------------------------------------------------ :
-


TrCHS3as  : ---------------------------------------------------------- :   -
TrCHScs   : AAAAAAAAAAAAAGTACTCTGCGTTGTTACCACTGCTTAATCACTAGTGAATTC : 2394
TrCHSfs   : ---------------------------------------------------------- :   -
TrCHShs   : ---------------------------------------------------------- :   -
```

TrLAR nucleotide sequence alignment

```
TrLARas : GAATTCGATTAAGCAGTGGTAACAACGCAGAGTACGCGGCG-----------------AT :
43
TrLARbs : GAATTCGATTAAGCAGTGGTAACAACGCAGAGTACGCGGCGAGGATCCTTCCATTTTGCAT :
60
TrLARcs : GAATTCGATTAAGCAGTGGTAACAACGCAGAGTACGCGGCG-----------------AT :
43

TrLARas : ACCAACATTGTCACAATTAACTCTAAAAGCAAAGCAATGGCACCAGCAGCAACATCATCA :
103
TrLARbs : ACCAACATTGTCACAATTAACTCTAAAAGCGAAAGCAATGGCACCAGCAGCAACATCATCA :
120
TrLARcs : ACCAACATTGTCACAATTAACTCTAAAAGCAAAAGCAATGGCACCAGCAGCAACATCATCA :
103

TrLARas : CCAACCACTCCTACTACTACCAAGGGTCGTGTCCTAATTGTTGGAGGAACAGGTTTCATT :
163
TrLARbs : CCAACCACTCCTACTACTACCAAGGGTCGTGTCCTAATTGTTGGAGGAACAGGTTTCATT :
180
TrLARcs : CCAACCACTCCCACTACTACCAAGGGTCGTGTCCTAATTGTTGGAGGAACAGGTTTCATT :
163

TrLARas : GGAAAATTTGTAACTGAGGCAAGTCTTTCCACAACACACCCAACCTACTTGTTGGTTCGG :
223
TrLARbs : GGAAAATTTGTAACTGAGGCAAGTCTTTCCACAACACACCCAACCTACTTGTTGGTTCGG :
240
TrLARcs : GGAAAATTTGTAACTGAGGCAAGTCTTTCCACAACACACCCAACCTACTTGTTGGTTCGG :
223

TrLARas : CCAGGACCTCTTCTCTCTTCTAAGGCTGCCACTATTAAGGCATTCCAAGAGAAAGGTGCC :
283
TrLARbs : CCAGGACCTCTTCTCTCTTCTAAGGCTGCCACTATTAAGGCATTCCAAGAGAAAGGTGCC :
300
TrLARcs : CCAGGACCTCTTCTCTCTTCTAAGGCTGCCACTATTAAGGCATTCCAAGAGAAAGGTGCC :
283

TrLARas : ATTGTCATTTATGGTCGGGTAAATAATAAGGAGTTCATGGAGATGATTTTGAAAAAGTAT :
343
TrLARbs : ATTGTCATTTATGGTCGGGTAAATAATAAGGAGTTCATGGAGATGATTTTGAAAAAGTAT :
360
TrLARcs : ATTGTCATTTATGGTCGGGTAAATAATAAGGAGTTCATGGAGATGATTTTGAAAAAGTAT :
343

TrLARas : GAGATAAATGTAGTCATTTCTGCAATAGGAGGCTCTGATGGCTTGCTGGAACAGCTTACT :
403
TrLARbs : GAGATAAATGTAGTCATTTCTGCAATAGGAGGCTCTGATGGCTTGCTGGAACAGCTTACT :
420
TrLARcs : GAGATAAATGTAGTCATTTCTGCAATAGGAGGCTCTGATGGCTTGCTGGAACAGCTTACT :
403

TrLARas : TTGGTGGAGGCCATGAAATCTATTAACACCATTAAGAGGTTTTTGCCTTCTGAATTTGGT :
463
TrLARbs : TTGGTGGAGGCCATGAAATCTATTAACACCATTAAGAGGTTTTTGCCTTCTGAATTTGGT :
480
TrLARcs : TTGGTGGAGGCCATGAAATCTATTAACACCATTAAGAGGTTTTTGCCTTCTGAATTTGGT :
463

TrLARas : CACGATGTGGACAGAGCAAATCCTGTGGAACCTGGCCTAACAATGTACAAACAGAAACGT :
```

```
523
TrLARas  :  CACGATGTGGACAGAGCAAATCCTGTGGAACCTGGCCTAACAATGTACAAACAGAAACGT  :
540
TrLARbs  :  CACGATGTGGACAGAGCACATCCTGTGGAACCTGGCCTAACAATGTACAAACAGAAACGT  :
523
TrLARcs  :  CACGATGTGGACAGAGCAGATCCTGTGGAACCTGGCCTAACAATGTACAAACAGAAACGT  :

TrLARas  :  TTGGTTAGACGTGTGATCGAAGAATCTGGTATACCATACACCTACATCTGTTGCAATTCG  :
583
TrLARbs  :  TTGGTTAGACGTGTGATCGAAGAATCTGGTGTACCATACACCTACATCTGTTGCAATTCG  :
600
TrLARcs  :  TTGGTTAGACGTGTGATCGAAGAATCTGGTATACCATACACCTACATCTGTTGCAATTCG  :
583

TrLARas  :  ATCGCATCTTGGCCGTACTATGACAATTGTCATCCATCACAGCTTCCTCCACCGTTGGAT  :
643
TrLARbs  :  ATCGCATCCTGGCCGTACTATGACAATTGTCATCCATCACAGCTTCCTCCACCGTTGGAT  :
660
TrLARcs  :  ATCGCATCTTGGCCGTACTATGACAATTGTCATCCATCACAGCTTCCTCCACCGTTGGAT  :
643

TrLARas  :  CAATTACATATTTATGGTCATGGCGATGTCAAAGCTTACTTTGTTGATGGCTATGATATT  :
703
TrLARbs  :  CAATTACATATTTATGGTCATGGCGATGTCAAAGCTTACTTTGTTGATGGCTATGATATT  :
720
TrLARcs  :  CAATTACATATTTATGGTCATGGCGATGTCAAAGCTTACTTTGTTGATGGCTATGATATT  :
703

TrLARas  :  GGGAAATTCACAATGAAGGTCATTGATGATGAAAGAACAATCAACAAAAATGTTCATTTT  :
763
TrLARbs  :  GGGAAATTCACAATGAAGGTCATTGATGATGAAAGAACAATCAACAAAAATGTTCATTTT  :
780
TrLARcs  :  GGGAAATTCACAATGAAGGTCATTGATGATGAAAGAACAATCAACAAAAATGTTCATTTT  :
763

TrLARas  :  CGACCTTCTAACAATTGTTATAGCATGAATGAGCTTGCTTCTTTGTGGGAAAACAAAATT  :
823
TrLARbs  :  CGACCTTCTAACAATTGTTATAGCATGAATGAGCTTGCTTCTTTGTGGGAAAACAAAATT  :
840
TrLARcs  :  CGACCTTCTAACAATTGTTATAGCATGAATGAGCTTGCTTCTTTGTGGGAAAACAAAATT  :
823

TrLARas  :  GCACGAAAAATTCCTAGAGTGACGTCGTCTCTGAAGACGATCTTCTAGCAATAGCCGCAGAA  :
883
TrLARbs  :  GCACGAAAAATTCCTAGAGTGACGTCGTCTCTGAAGACGATCTTCTAGCAATAGCCGCAGAA  :
900
TrLARcs  :  GCACGAAAAATTCCTAGAGTGACGTCGTCTCTGAAGACGATCTTCTAGCAATAGCCGCAGAA  :
883

TrLARas  :  AAATGCATACCGGAAAGTGTTGTGGCACCAATCACTCATGATATATTCATCAATGGATGT  :
943
TrLARbs  :  AACTGCATACCGGAAAGTGTTGTGTGGCATCAATCACTCATGATATATTCATCAATGGATGT  :
960
TrLARcs  :  AATTGCATACCGGAAAGTGTTGTGGCACCAATCACTCATGATATATTCATCAATGGATGT  :
943

TrLARas  :  CAAGTTAACTTCAAGATAGATGGAATTCATGATGTTGAAATTGGCACTCTATATCCTGGT  :
1003
TrLARbs  :  CAAGTTAACTTCAAGGTAGATGGAATTCATGATGTTGAAATTGGCACTCTATATCCTGGT  :
1020
```

```
TrLARcs : CAAGTTAACTTCAAGATAGATGGAATTCATGATGTTGAAATTGGCACTCTATATCCTGGT :
1003

TrLARas : GAATCGGTAAGAAGTTTGGAGGAATGCTATGAGAAATTTGTTGTCATGGCGGCTGACAAG :
1063
TrLARbs : GAATCGGTAAGAAGTTTGGAGGAATGCTATGAGAAATTTGTTGTCATGGCGGCTGACAAG :
1080
TrLARcs : GAATCGGTAAGAAGTTTGGAGGAATGCTATGAGAAATTTGTTGTCATGGCGGCTGACAAG :
1063

TrLARas : ATTCATAAAGAAGAAACTGGAGTTACCGCAGGTGGGGCGGCACAACGGCTATGGTAGAG :
1123
TrLARbs : ATTCATAAAGAAGAAACTGGAGTTACCGCAGGTGGGGCGGCACAACGGCTATGGTAGAG :
1140
TrLARcs : ATTCATAAAGAAGAAACTGGAGTTACCGCAGGTGGGGCGGCACAACGGCTATGGTAGAG :
1123

TrLARas : CCGGTGCCAATCACAGCTTCCTGTTGAAAAGGTTCACCTGAGGTGGATATTCTTTTGAGT :
1183
TrLARbs : CCGGTGCCAATCACAGCTTCCTGTTGAAAAGGTTCACCTGAGGTGGATATTCTTTTGAGT :
1200
TrLARcs : CCGGTGCCAATCACAGCTTCCTGTTGAAAAGGTTCACCTGAGGTGGATATTCTTTTGAGT :
1183

TrLARas : CATAAGACATGTTGATTGTTGATGTTGTTTTCAAGAATGTTTCATCATTTCATGTGTTTT :
1243
TrLARbs : CATAAGACATGTTGATTGTTGATGTTGTTTTCAAGAATGTTTCATCATTTCATGTGTTTT :
1260
TrLARcs : CATAAGACATGTTGATTGTTGATGTTGTTTTCAAGAATGTTTCATCATTTCATGTGTTTT :
1243

TrLARas : ATTAATCCTAAGTACAAATAATTGCTGTCTACGTACGTTCTTAGTTGCAAAAATTCTTGT :
1303
TrLARbs : ATTAATCCTAAGTACAAATAATTGCTGTCTACGTACGTTCTTAGTTGCGAAAATTCTTGT :
1320
TrLARcs : ATTAATCCTAAGTACAAATAATTGCTGTCTACGTACGTTCTTAGTTGCAAAAATTCTTGT :
1303

TrLARas : TATTCTCTATTGAGGTAAAACTCTTCATGTTTAC---------------------------- :
1337
TrLARbs : TATTCTCTATTGGGGTAAAAGTCTTCATGTTTATTGTAGTTGTGTTGGTTTTTCATATAT :
1380
TrLARcs : TATTCTCTATC------------------------------------------------- :
1314

TrLARas : ------------------------------------------------------------ :
-
TrLARbs : GCTATTTGCAATAATGATTTTTGTGAAGCACTTGTGGTGTATTTACTTACTACTGAAAAT :
1440
TrLARcs : ------------------------------------------------------------ :
-

TrLARas : ----------------------------------------AAAAAAAAAAAAAAAAAAAA :
1358
TrLARbs : AATGGTTACACAAAATATATAAAAAAATAAAAATAAGCAAAAAAAAAAAAAAAAAAAAAA :
1500
TrLARcs : ----------------------------------------AAAAAAAAAA-AAAAAAAAA :
1333

TrLARas : AAAAAAAAAAGTACTCTGCGTTGTTACCACTGCTTAATCACTAGTGAATTC : 1409
```

```
TrLARbs : AAAAAAAAAAGTACTCTGCGTTGTTACCACTGCTTAATCACTAGTGAATTC : 1551
TrLARcs : AAAAAAAAAAGTACTCTGCGTTGTTACCACTGCTTAATCACTAGTGAATTC : 1384
```

TrCHS amino acid sequence alignment

```
TrCHS3ap  : MVSVAEIRKAQ----------RAECPATILAIGTANPNRVEQSTYPDFYFRITNSEHKTEL
: 52
TrCHScp   : MGDEGIVRG--------VTKQTEPGKATILAIGKAEPHOLVMQECLVEGYFRDTNCDN-PEL
: 53
TrCHSfp   : -MPQGDENGSSSVNGARARRAPLOGKATILALGKAEEAQVLPQECLVEGEIRDIKCDD-LYI
: 60
TrCHShp   : VVTVEEIRNAQ----------RSNGPATILAEGTATESNCVTQADYPEYYFRITNSEHMTDL
: 52

TrCHS3ap  : KEKFQRMCDKSMIKRRYMYLTEEILKENPSLCEYMAPSLDARQDVVVEYPRLGKEAAVKAI
: 114
TrCHScp   : KQRLARLCKTTTVKTRYMVMNEEILKKYPEIVVEGNSTVKQRLEICNEAVTQYAIEASQVCE
: 115
TrCHSfp   : KEKLERLCKNTTVKTRYTVMSKEILDNYEPLAIDGTHTIRQKLEIANPAMVEVATRASKDCI
: 122
TrCHShp   : KEKEFRMCDRSMIKKRYMHLTEDELKENPNMCEYMAPSIDVRRDIVVVEVPRLGKFAAKKAI
: 114

TrCHS3ap  : KEWGQPKSKITHLIECTTSGVDMPGYDYQLIKLLGLREYVKRYMMYQQGCFAGGIVLRLAKD
: 176
TrCHScp   : KNWGRSLSDITHVVYVSSSEARLPGGDLYLSKGLGINEKIQRTMLYESSCSGGVAGLRVAKD
: 177
TrCHSfp   : KIWGRSPQDITHIVYVSSSPTRLPGGDLYLANELGLNSDVNRVMLYPLGCYGGVTGLRVAKD
: 184
TrCHShp   : CEWGQPKSKITHLVFCTTSGVDMPGYDYQLTKLLGLRSVKRLMMYQQGCFAGGIVLRLAKD
: 176

TrCHS3ap  : LAENNKGARVLVVCSEVTAVTFRGPSDTHLDSLVGQALFGDGAFALIVGSDPYPEIEKPIIE
: 238
TrCHScp   : VAENNPESRVLLATSETTIIGFKPPSVDRPYDLVGVALFGDGAAMIIGJDPVFETETELFE
: 239
TrCHSfp   : IAENNPESRVLLTTSETTILGFRPPSKARPYDLVGAALFGDGAAAIIGTDPTLNQESFME
: 246
TrCHShp   : TVENNKNARVLVVCSETTAVTFRGPSDTHLDSLVGQALFGDGAAAMIIGADPDLTVERPIFE
: 238

TrCHS3ap  : VVWTAQTIAPDSEGAIDGHLREAGLTFHLLKDVPGTVSKNINKALVEAFQPLG--TSDYNSI
: 298
TrCHScp   : LHTSHQEFIPDTEKFIDGRITBEGIGFTIANELPQIEDNVPGFCNKLIDVVGSLENKEYNKL
: 301
TrCHSfp   : LNHAVQKPLPDTQNVIDGRITEEGINEKIGRDLPQKIEDNIEEFCKKIMAKS--DVKEFNDL
: 306
TrCHShp   : TVSAAQTILPDSDGAIDGHLREVGLTFHLLKDVPGTISKNIFKSLVEAFAPIG--INDWNSI
: 298

TrCHS3ap  : EWIAHPGGPAILQVEQKLALKPEKMRATREVLSEYGNMSSACVLFILDEMKKSAQNGLKT
: 360
TrCHScp   : FWAVHPGGPAILNRVEKTLPLSPCKINASRKALMDYGNASSNTIVYVLEYMLEEEKKI-KKA
: 362
TrCHSfp   : FWAVHPGGPAILNKLENIKLKSDKLDCSRKALMDYGNVSSNTEFYVMEYMKDYLK-----E
: 363
TrCHShp   : FWVAHPGGPAILDQVEEKIHLKPEKLKLRSTRHVLSEYGNMSSACVLFILDEMEKRSKEEGMIT
: 360

TrCHS3ap  : TCEGLDWGVLPGFGPGLTIETVVGRSVAI-- : 389
TrCHScp   : GQGDSEVWGLILAFGPGITEEGIIARNMCA-- : 391
TrCHSfp   : -DGSPEWGLGIAFGPGITEEGVLLRSI---- : 389
```

TrCHShp   : TGEGLEWGVIFGFGPGLIVETVVIHSVPVQG : 391

TrLAR amino acid sequence alignment

```
TrLARap  : MAPAATSSPTTPTTTKGRVLIVGGTGFIGKFVTEASLSTTHPTYLLVRPGPLLSSKAATI :
60
TrLARbp  : MAPAATSSPTTPTTTKGRVLIVGGTGFIGKFVTEASLSTTHPTYLLVRPGPLLSSKAATI :
60
TrLARcp  : MAPAATSSPTTPTTTKGRVLIVGGTGFIGKFVTEASLSTTHPTYLLVRPGPLLSSKAATI :
60

TrLARap  : KAFQEKGAIVIYGRVNNKEFMEMILKKYEINVVISAIGGSDGLLEQLTLVEAMKSINTIK :
120
TrLARbp  : KAFQEKGAIVIYGRVNNKEFMEMILKKYEINVVISAIGGSDGLLEQLTLVEAMKSINTIK :
120
TrLARcp  : KAFQEKGAIVIYGRVNNKEFMEMILKKYEINVVISAIGGSDGLLEQLTLVEAMKSINTIK :
120

TrLARap  : RFLPSEFGHDVDRANPVEPGLTMYKQKRLVRRVIEESGIPYTYICCNSIASWPYYDNCHP :
180
TrLARbp  : RFLPSEFGHDVDRANPVEPGLTMYKQKRLVRRVIEESGVPYTYICCNSIASWPYYDNCHP :
180
TrLARcp  : RFLPSEFGHDVDRADPVEPGLTMYKQKRLVRRVIEESGIPYTYICCNSIASWPYYDNCHP :
180

TrLARap  : SQLPPPLDQLHIYGHGDVKAYFVDGYDIGKFTMKVIDDERTINKNVHFRPSNNCYSMNEL :
240
TrLARbp  : SQLPPPLDQLHIYGHGDVKAYFVDGYDIGKFTMKVIDDERTINKNVHFRPSNNCYSMNEL :
240
TrLARcp  : SQLPPPLDQLHIYGHGDVKAYFVDGYDIGKFTMKVIDDERTINKNVHFRPSNNCYSMNEL :
240

TrLARap  : ASLWENKIARKIPRVIVSEDDLLAIAAENCIPESVVAPITHDIFINGCQVNFKIDGIHDV :
300
TrLARbp  : ASLWENKIARKIPRVIVSEDDLLAIAAENCIPESVVASITHDIFINGCQVNFKVDGIHDV :
300
TrLARcp  : ASLWENKIARKIPRVIVSEDDLLAIAAENCIPESVVA ITHDIFINGCQVNFKIDGIHDV :
300

TrLARap  : EIGTLYPGESVRSLEECYEKFVVMAADKIHKEETGVTAGGGGTTAMVEPVPITASC : 356
TrLARbp  : EIGTLYPGESVRSLEECYEKFVVMAADKIHKEETGVTAGGGGTTAMVEPVPITASC : 356
TrLARcp  : EIGTLYPGESVRSLEECYEKFVVMAADKIHKEETGVTAGGGGTTAMVEPVPITASC : 356
```